



SEQUENCE LISTING

<110> MacPhee, Colin Houston  
Tew, David Graham  
Southan, Christopher Donald  
Hickey, Deirdre Mary Bernadette  
Gloger, Israel Simon  
Lawrence, Geoffrey Mark Prouse  
Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,  
Inhibitors Thereof and Use of the Same in Diagnosis and  
Therapy

<130> P30693C4X1C1

<140> 09/922,067  
<141> 2001-08-03

<150> 09/193,130  
<151> 2000-11-28

<150> 08/387,858  
<151> 1994-06-24

<150> PCT/GB94/01374  
<151> 1994-06-24

<150> GB 9313144.9  
<151> 1993-06-25

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Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His  
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Lys Asp Phe Asp Gln  
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Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro  
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Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn  
20 25 30

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Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His  
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Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly  
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Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr

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10

15

Pro Ala Asn

<210> 5

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<212> DNA

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<221> misc\_feature

<222> 265, 390, 395, 403, 406

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gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctccttcaat 120  
caagcagtc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180  
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240  
catgtgtcca attatcttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300  
acccttgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360  
gatattagca ggatattgga aatattcagn gttgntaaaa agnggnggct gagggattct 420

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<211> 379

<212> DNA

<213> Unknown

<220> Homo sapien

<221> misc\_feature

<222> 84

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tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
caaagcttca ttagcattct tacaaaagca tttaggactt cataaagatt ttgttcagtg 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccagggaa taggaggaaa tacaattggg 360
gtttaaaata ggttttttt 379

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<222> 257

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agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
agtatattcc agaattcctc agcccctctt ttttatcaac tctgaatatt tccaatatcc 240
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<213> Homo sapien

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gtatattcca gaattcctca gcccctcttt tttatcaact ctgaatattt ccaatattct 180
gctaatatca taaaaatgaa aaaatgctac tcacctgata aagaaagaaa gatgattaca 240
atcagggggt cagtcacca gaattttgct gacttcactt ttgcaactgg caaaataatt 300
ggacacatgc tcaaattaa gggagacata gattcaaatt tagctattga tcttagcaac 360
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaaat 540
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1 5

cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt 103  
His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe  
10 15 20

gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg 151  
Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp  
25 30 35

gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act 199  
Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr  
40 45 50

aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgt aca gac tta 247  
Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu  
55 60 65 70

atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca 295  
Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro  
75 80 85

tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa 343  
Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu  
90 95 100

tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc 391

Tyr	Phe	Trp	Gly	Leu	Ser	Lys	Phe	Leu	Gly	Thr	His	Trp	Leu	Met	Gly	
	105						110					115				
aac	att	ttg	agg	tta	ctc	ttt	ggg	tca	atg	aca	act	cct	gca	aac	tgg	439
Asn	Ile	Leu	Arg	Leu	Leu	Phe	Gly	Ser	Met	Thr	Thr	Pro	Ala	Asn	Trp	
	120						125					130				
aat	tcc	cct	ctg	agg	cct	ggg	gaa	aaa	tat	cca	ctt	gtt	gtt	ttt	tct	487
Asn	Ser	Pro	Leu	Arg	Pro	Gly	Glu	Lys	Tyr	Pro	Leu	Val	Val	Phe	Ser	
	135					140				145				150		
cat	ggg	ctt	ggg	gca	ttc	agg	aca	ctt	tat	tct	gct	att	ggc	att	gac	535
His	Gly	Leu	Gly	Ala	Phe	Arg	Thr	Leu	Tyr	Ser	Ala	Ile	Gly	Ile	Asp	
			155					160					165			
ctg	gca	tct	cat	ggg	ttt	ata	gtt	gct	gct	gta	gaa	cac	aga	gat	aga	583
Leu	Ala	Ser	His	Gly	Phe	Ile	Val	Ala	Ala	Val	Glu	His	Arg	Asp	Arg	
			170					175					180			
tct	gca	tct	gca	act	tac	tat	ttc	aag	gac	caa	tct	gct	gca	gaa	ata	631
Ser	Ala	Ser	Ala	Thr	Tyr	Tyr	Phe	Lys	Asp	Gln	Ser	Ala	Ala	Glu	Ile	
	185						190					195				
ggg	gac	aag	tct	tgg	ctc	tac	ctt	aga	acc	ctg	aaa	caa	gag	gag	gag	679
Gly	Asp	Lys	Ser	Trp	Leu	Tyr	Leu	Arg	Thr	Leu	Lys	Gln	Glu	Glu	Glu	
	200						205				210					
aca	cat	ata	cga	aat	gag	cag	gta	cgg	caa	aga	gca	aaa	gaa	tgt	tcc	727
Thr	His	Ile	Arg	Asn	Glu	Gln	Val	Arg	Gln	Arg	Ala	Lys	Glu	Cys	Ser	
	215				220				225				230			
caa	gct	ctc	agt	ctg	att	ctt	gac	att	gat	cat	gga	aag	cca	gtg	aag	775
Gln	Ala	Leu	Ser	Leu	Ile	Leu	Asp	Ile	Asp	His	Gly	Lys	Pro	Val	Lys	
			235					240					245			
aat	gca	tta	gat	tta	aag	ttt	gat	atg	gaa	caa	ctg	aag	gac	tct	att	823
Asn	Ala	Leu	Asp	Leu	Lys	Phe	Asp	Met	Glu	Gln	Leu	Lys	Asp	Ser	Ile	
		250					255					260				
gat	agg	gaa	aaa	ata	gca	gta	att	gga	cat	tct	ttt	ggg	gga	gca	acg	871

Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr	
265	270 275
gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc	919
Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala	
280	285 290
ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att	967
Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile	
295	300 305 310
cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct	1015
Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala	
	315 320 325
aat atc ata aaa atg aaa aaa tgc tac tca cct gat aaa gaa aga aag	1063
Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys	
	330 335 340
atg att aca atc agg ggt tca gtc cac cag aat ttt gct gac ttc act	1111
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr	
	345 350 355
ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac	1159
Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp	
	360 365 370
ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca	1207
Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala	
	375 380 385 390
ttc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac	1255
Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp	
	395 400 405
tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att	1303
Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile	
	410 415 420
aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag	1351

Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu  
425 430 435

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Lys Tyr Asn  
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Gln Tyr Ile Asn Pro Val Ala  
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Phe Ala Thr Gly  
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Gln Tyr Ile Asn Pro

1

5

1/6